

FIGURE 1A

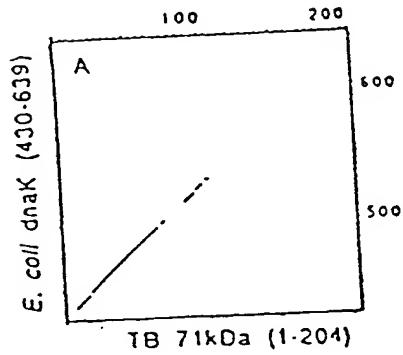
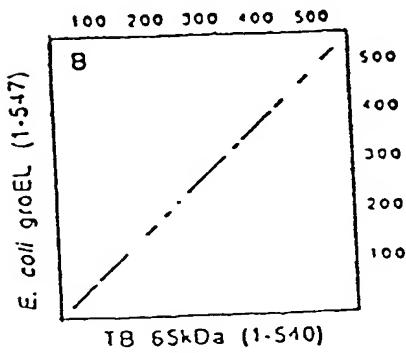


FIGURE 1B



	1	10	20	30	40	50	60	70
HUMPI	MLRLPTVFRQMRPVSRLAPHLTRAYAKDVKGADARALMLQGV DLLADAVAVTMGPKGRTVIIIEQSWGS							
GROEL	-----MA-----AKDVKGNDARVKMLRGVNVLADAVKVLGPKGRNVVLDKSFGA							
	71	80	90	100	110	120	130	140
HUMPI	PKVTKDGVTVAKSIDLKDVKNIGAKLVQDVANNTNEEAGDGTTATVLARSIAKEGFEXKISKGANPVEI							
GROEL	PTITKDGVSVAREIEPEDKFENMGAQMVKEVASKANDAAGDGTTATVLAQAIITEGLKAVAAGMNPMDL							
	141	150	160	170	180	190	200	210
HUMPI	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVIITVKDGKTLNDE							
GROEL	KRGIDKAVTAAVEELKALSVPCSDSKAIAQVGTISANSDETVGKLIAEAMDVKVGKEGVITVEDGTGLQDE							
	211	220	230	240	250	260	270	280
HUMPI	LEIIIEGMKFDRGYIISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIIAEDVDG							
GROEL	LDVVEGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIIAEDVEG							
	281	290	300	310	320	330	340	350
HUMPI	EALSTLVLNRLKVGQLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEGLTLNLEDVQPHDLGKVGEVIV							
GROEL	EARLATAVVNTIRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEE-IGMELEKATLEDLGQAKRVVI							
	351	360	370	380	390	400	410	420
HUMPI	TKDDAMLLKGKGDKAQIEKRIQEIIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSVDVEVNEKKDF							
GROEL	NKDTTTIIDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKAF							
	421	430	440	450	460	470	480	490
HUMPI	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSL							
GROEL	VEDALHATRAAVEEGVVAGGGVALIRVASKLADLRGQNEDQNVVSSL-RAMEAPLRQIVLNCGEEPSV							
	491	500	510	520	530	540	550	56
HUMPI	VEKIMQSSSEVGYDAMAGDFVNMEVKIDPTKVVRTALLDAAGVASLLTAEVVVTEIPKEEKDPGMG							
GROEL	ANTVKGGDGNYGYNAATEEYGNMIDMGILDPTKVTRSALQYAASVAGLMITTECNVTDLPKND-AADLG							
	561	570						
HUMPI	MGGMGG--GMGGGMF							
GROEL	AGGMGGMGGMGGMM-							

Total score = 4667, 5 breaks
 276 identities out of 545 possible matches between residues

25 random runs
 Alignment score = 65.34 SD Standard deviation = 18.94 Mean = 3429.48

	1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRLAPHLTRAYAKDVKGADARALMLQGVVDLLADAVAVTMGPKGRTVIEQSWGS							
HL65K	M-----AKTIAVDEEARRGLERGLNSLADAVKVTLGPKGRNVVLEKKWGA							
	71	80	90	100	110	120	130	140
HUMP1	PKVTKDGTVAKSIDLKDKYKNIGAKLVQDVANNNTNEEAGDGTTATVLARSIAKEGFEKISKGANPVEI							
HL65K	PTITNDGVSIAKIEIELEDPYEKIGAELVKEVAKKIDDVAGDGTTATVLAQALVKEGLRNVAAGANPLGL							
	141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVIIVKDGKTLNDE							
HL65K	KRGIEKAVDKVTETLLKDAKEVETKEQIAATAAISA-GDQSIGDLIAEAMDKVGNEGVITVEESNTFGLQ							
	211	220	230	240	250	260	270	280
HUMP1	LEIIEGMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSEQSIVPALEIANAHRKPLVIIAEDVDG							
HL65K	LELTEGMRFDKGYISGYFVTDAERQEAVLZEPYILLVSSKVSTVKDLPPLERVIQAGKSLLIIAEDVVEG							
	281	290	300	310	320	330	340	350
HUMP1	EALSTLVLNRLKVGLQVVAVKAPGFGDNRKNQLKDMIAITGGAVFGEEGLTINLEDVQPHDLGKVGEIV							
HL65K	EALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMAILTGAQVISEE-VGLTLENTDLSLLGKARKVVM							
	351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKGKGDKAQIEKRIQEIIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGCGTSDVEVNEKKDR							
HL65K	TKDETTIVEGAGDTDAIAGRVAQIRTEIENSDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHR							
	421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLI							
HL65K	IEDAVRNAKAAVEEGIVAGGGVTLLQAAPALDKLKLTGDEAT-GANIVKVALEAPLKQIAFNSGMEPGV							
	491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSSEVGYDAMAGDFVNMFVEKGIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKD?GMG							
HL65K	AEKVRNLSQLVGHGLNAATGEYEDLLKAGVADPVKVTRSALQNAASIAGLFTT-EAVVADKPEKTAAPASD							
	561	570						
HUMP1	MGGMGGGMGGGMF							
HL65K	TGGMGG-MD---?							

Total score - 4552, 7 breaks

255 identities out of 540 possible matches between residues

25 random runs
Alignment score = 47.73 SD Standard deviation = 23.86 Mean = 3413.15

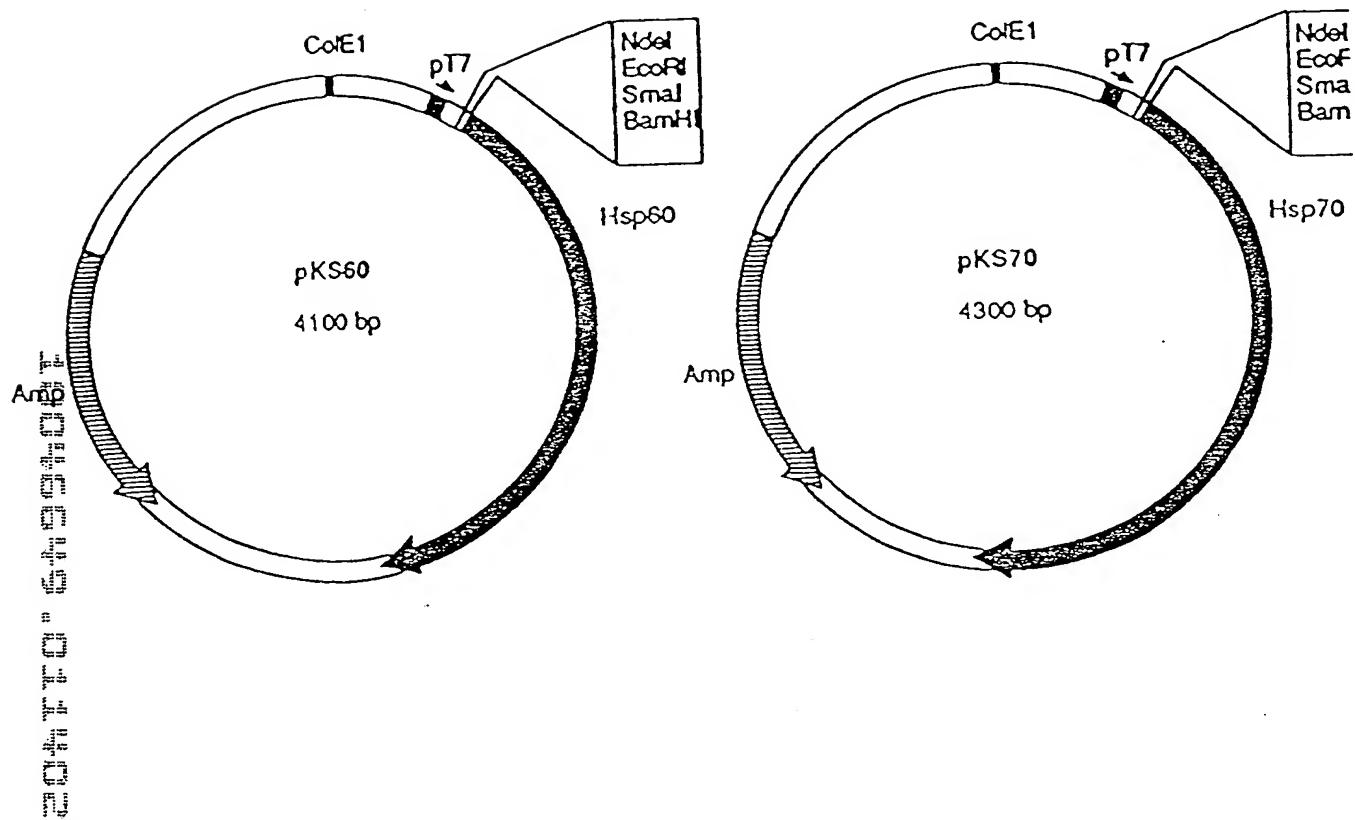
FIGURE 4

	10	20	30	40	50	60	70
HUMPL	MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKGADARALMLOGV DLLADAVAVTMGPKGRTVIIIEQSNGS						
T365K	-----AKTIAYDEEARRGLERGLNALADAVKVTLGPKGRNVVLEKKWGP						
	71	80	90	100	110	120	130
HUMPL	PKVTKDGTVAKSIDLKDKYKNIGAKLVQDVANNNTNEEAGDGTTATVLARSIAKEGFEKISKGANPVEI						
T365K	PTITNDGVSIAKEIELEDPYEKIGAELVKEAKTDDVAGDGTTATVLAQALRKEGLRNVAAGANPLGI						
	141	150	160	170	180	190	200
HUMPL	RRGVMLAVDAVIAELKKQSVPVTPPEEIAQVATISANGDKEIGNIISDANKVGRKGVITVKDGKTLND						
T365K	KGIEKAVEKVETETLLKGAKEVETKEQIAATAAISA-GDQSIGDLIAEAMDKGVGNEGVTVEESNTFGL						
	211	220	230	240	250	260	270
HUMPL	LEIIEGMKFDRGYIISPYFINTSKGQKCEQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVD						
T365K	LELTEGMRFDKGYIISGYFVTDPERQEAVIDPYILLVSSKVSTVKDLLPLLEKVIGAGKPLLIIAEDVE						
	281	290	300	310	320	330	340
HUMPL	EALSTLVNLXVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEGLTLNLEDVQPHDLGVGEVI						
T365K	EALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMAILTGGQVISEE-VGLTLENADLSLLGKAKKV						
	351	360	370	380	390	400	410
HUMPL	TKDDAMLLKGKGDKAQIEKRIQEIIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGSIDVEVNEKKD						
T365K	TKDETTIVEGAGDTDIAIGRVAQIRQEIEIENSDSDYDREKLQERLAKLAGGVAVIKAGAAATEVELKERKH						
	421	430	440	450	460	470	480
HUMPL	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVESSI						
T365K	IEDAVRNAKAAVEEGIVAGGGVTLIQAAPTLDELK-LEGDEATGANIVKVALEAPLKQIAFNSGLEPGI						
	491	500	510	520	530	540	550
HUMPL	VEKIMQSSSEVGYDAMAGDFVNVMVEKGIIIDPTKVVRTALLDAAGVASLLTAEVVVTEIPKEEKDPGM						
T365K	AEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSALQNAASIAGLFLTTEAVVADKPEKEKASVP						
	561	570					
HUMPL	MGGMGGGMGGMF						
T365K	----GGDMGGMDF						

Total score - 4360, 5 breaks
257 identities out of 340 possible matches between residues

25 random runs Standard deviation - 23.23 Mean - 3413.15
Alignment score - 49.36 SD

Figure 5



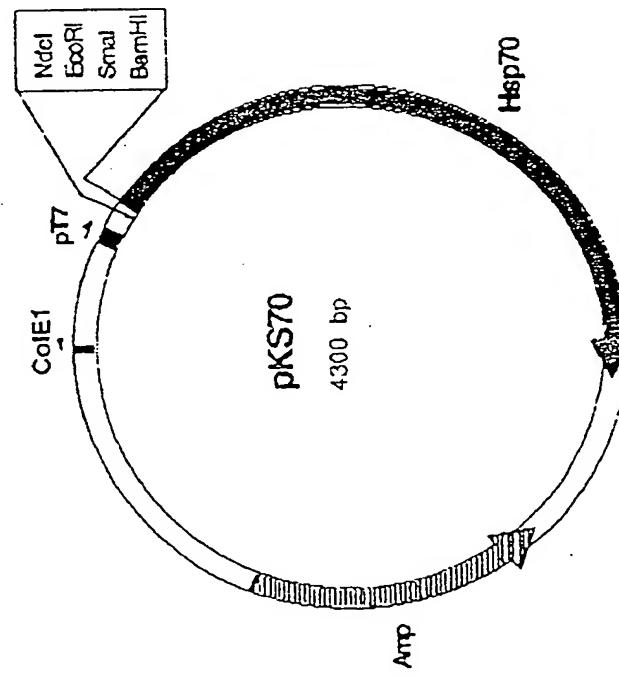
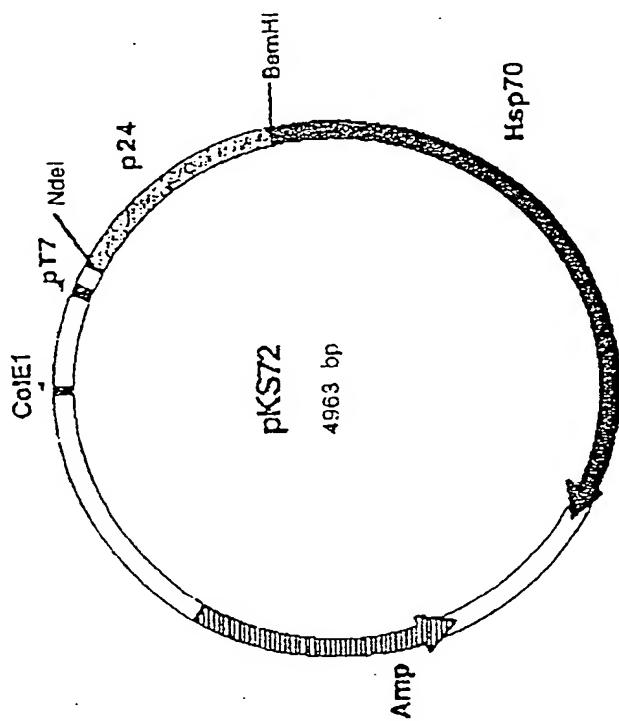


FIGURE 6

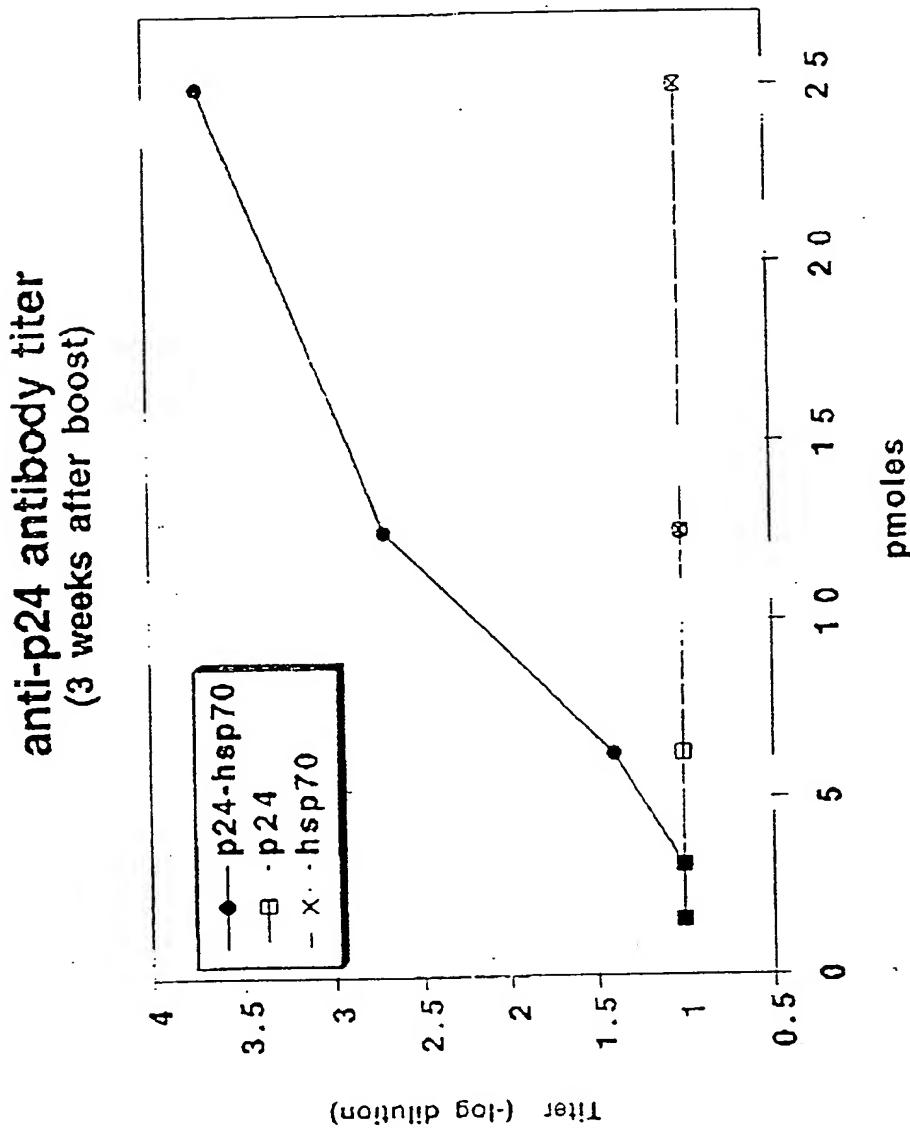


FIGURE 7